

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.

Application Serial Number: 10/510,959  
Source: PT/10  
Date Processed by STIC: 11/8/04

# ***ENTERED***



PCT

## RAW SEQUENCE LISTING

DATE: 11/08/2004

PATENT APPLICATION: US/10/510,959

TIME: 12:01:10

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\11082004\J510959.raw

4 <110> APPLICANT: Lovejoy, David  
 6 Chewpoy, R.B.  
 8 Barsyte, Dalia  
 10 Rotzinger, Susan  
 13 <120> TITLE OF INVENTION: Tereuin C-Terminal Associated Peptides (TCAP) And Methods  
 And Uses  
 14 Thereof  
 16 <130> FILE REFERENCE: 2223-189  
 C--> 19 <140> CURRENT APPLICATION NUMBER: US/10/510,959  
 C--> 21 <141> CURRENT FILING DATE: 2004-11-01  
 24 <150> PRIOR APPLICATION NUMBER: US 60/376,879  
 26 <151> PRIOR FILING DATE: 2002-05-02  
 30 <150> PRIOR APPLICATION NUMBER: US 60/377,231  
 32 <151> PRIOR FILING DATE: 2002-05-03  
 36 <150> PRIOR APPLICATION NUMBER: US 60/424,016  
 38 <151> PRIOR FILING DATE: 2002-11-06  
 42 <160> NUMBER OF SEQ ID NOS: 136  
 46 <170> SOFTWARE: PatentIn version 3.1  
 50 <210> SEQ ID NO: 1  
 52 <211> LENGTH: 1490  
 54 <212> TYPE: DNA  
 56 <213> ORGANISM: Artificial Sequence  
 60 <220> FEATURE:  
 62 <223> OTHER INFORMATION: Rainbow Trout Ten M3 carboxy termini'  
 64 <400> SEQUENCE: 1  
 65 tccatctcgg ggggtgcaaca ggaagtgacc cggcaagcca aggcctttcct gtccttcgag 60  
 67 aggatgcccg agatccagct gagccgccgg cgctccaacc gggagaaaacc ctggctgtgg 120  
 69 ttcgccaccg ccaagtctct gatcggtaag ggtgtcatgt tggcgggtgac gcagggccgt 180  
 71 gtggtcacca acgctctgaa catcgccaac gaggactgca tcaaggctgc cgccgtcctc 240  
 73 aacaatgcgt tctacctgga ggacctgcac ttcacgggtg agggacgcga cacgcactac 300  
 75 ttcacaaaga ccagcctccc ggagagcgac ctgggagcgc tgaggctgac aagcgggagg 360  
 77 aagtcgctgg agaacggaag tcaacgtgac tgtgtcccag tccaccaccg tgggtgaacgg 420  
 79 cagaaccggc gcttcgccga cgtggagctg cagtacggcg ctctagcgtc ccacgtgcgc 480  
 81 tatggcatga ctctggacga ggagaaggcg cgtgtgctgg agcaggccag gcagaaggcg 540  
 83 ttgtcgagtg cctgggtccag ggagcaacaa cgggtgaggg agggggagga ggggggtgagg 600  
 85 ctgtggacgg agggggagaa gaggcagctg ctgagcggga ggaaggttct gggctacgac 660  
 87 gggactacg tcctctccat agagcagtag cccgagctag cagactccgc taacaacatc 720  
 89 cagttcctca ggcagagcga aataggggaag aggtaacaga cagaatcctc ggactggcc 780  
 91 gccaaagaga ctacccctc caaatcctgc cccccaacct ccctcgcctc ccccttttc 840  
 93 tctaaaaagg gggagggtcc aggctagtgc tgtgttttag gccgactagc tgaaacaaac 900  
 95 agtaaaatgt agaatatctt aaactgaact atacctaata ctaccactgt ggggcctgaa 960  
 97 aatcaaacaa aacggtctca actgacgcaa atgtttgtcc catgtgctat acagcgttga 1020  
 99 atggactgtg gactctcttg aaaagagaga aaaaaaagtc aaaactctcg gtttgtgaaa 1080  
 101 ggagaaaaaa acgttttttt tttttttaaa tagacttcct gaatttgctt tcggaaaaaa 1140

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103 tatttttaaaa agaaagaaga aatgtgttta catacgcata acactacaac acgtctggac 1200
105 taatagaaga aaagccttct ggtttcttac acaggacaac gtctataatc tgattctaca 1260
107 tcctgacgac tgacctttga ttgacctttg cgtactgaaa aaggtagtgt tgttgttcgc 1320
109 agtaggacca tgggtctcca atggtggtaa ctagacagtt aaaaccactt gttgaaacca 1380
111 cttgcttggt cttctgcttt tctttccaaa agggacaaaa cagctcccac caagtgactt 1440
113 ctttaccaat actagatcaa agtgggacgt tttgggctcg tgccgaattc 1490

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116 &lt;210&gt; SEQ ID NO: 2

118 &lt;211&gt; LENGTH: 756

120 &lt;212&gt; TYPE: DNA

122 &lt;213&gt; ORGANISM: Artificial Sequence

126 &lt;220&gt; FEATURE:

128 <223> OTHER INFORMATION: Rainbow Trout Ten M3 coding sequence of carboxy termini of  
Ten M3

130 &lt;400&gt; SEQUENCE: 2

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131 tccatctcgg ggggtcaaca ggaagtgacc cggcaagcca aggctttcct gtccttcgag 60
133 aggatgccgg agatccagct gagccgccgg cgctccaacc gggagaaacc ctggctgtgg 120
135 ttcgccaccg ccaagtctct gatcggtaag ggtgtcatgt tggcggtgac gcagggccgt 180
137 gtggtcacca acgctctgaa catcgccaac gaggactgca tcaaggctcg cgccgtcctc 240
139 aacaatgcgt tctacctgga ggacctgcac ttcacgggtg agggacgcga cacgcactac 300
141 ttcatcaaga ccagcctccc ggagagcgac ctgggagcgc tgaggctgac aagcgggagg 360
143 aagtcgctgg agaacggaag tcaacgtgac tgtgtcccag tccaccaccg tggngaacgg 420
145 cagaaccggc gcttcgccga cgtggagctg cagtacggcg ctctagcgct ccacgtgcgc 480
147 tatggcatga ctctggacga ggagaaggcg cgtgtgctgg agcaggccag gcagaaggcg 540
149 ttgtcgagtg cctggtccag ggagcaacaa cgggtgaggg agggggagga gggggtagg 600
151 ctgtggacgg agggggagaa gaggcagctg ctgagcggga ggaaggttct gggctacgac 660
153 gggtagctac tcctctccat agagcagtag cccgagctag cagactccgc taacaacatc 720
155 cagttcctca ggcagagcga aatagggaag aggttaa 756

```

158 &lt;210&gt; SEQ ID NO: 3

160 &lt;211&gt; LENGTH: 251

162 &lt;212&gt; TYPE: PRT

164 &lt;213&gt; ORGANISM: Artificial Sequence

168 &lt;220&gt; FEATURE:

170 &lt;223&gt; OTHER INFORMATION: Rainbow Trout Ten M3 carboxy termini of Ten M3

172 &lt;400&gt; SEQUENCE: 3

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174 Ser Ile Ser Gly Val Gln Gln Glu Val Thr Arg Gln Ala Lys Ala Phe
175 1 5 10 15
178 Leu Ser Phe Glu Arg Met Pro Glu Ile Gln Leu Ser Arg Arg Arg Ser
179 20 25 30
182 Asn Arg Glu Lys Pro Trp Leu Trp Phe Ala Thr Ala Lys Ser Leu Ile
183 35 40 45
186 Gly Lys Gly Val Met Leu Ala Val Thr Gln Gly Arg Val Val Thr Asn
187 50 55 60
190 Ala Leu Asn Ile Ala Asn Glu Asp Cys Ile Lys Val Ala Ala Val Leu
191 65 70 75 80
194 Asn Asn Ala Phe Tyr Leu Glu Asp Leu His Phe Thr Val Glu Gly Arg
195 85 90 95
198 Asp Thr His Tyr Phe Ile Lys Thr Ser Leu Pro Glu Ser Asp Leu Gly
199 100 105 110
202 Ala Leu Arg Leu Thr Ser Gly Arg Lys Ser Leu Glu Asn Gly Val Asn
203 115 120 125

```

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```

206 Val Thr Val Ser Gln Ser Thr Thr Val Val Asn Gly Arg Thr Arg Arg
207      130      135      140
210 Phe Ala Asp Val Glu Leu Gln Tyr Gly Ala Leu Ala Leu His Val Arg
211 145      150      155      160
214 Tyr Gly Met Thr Leu Asp Glu Glu Lys Ala Arg Val Leu Glu Gln Ala
215      165      170      175
218 Arg Gln Lys Ala Leu Ser Ser Ala Trp Ser Arg Glu Gln Gln Arg Val
219      180      185      190
222 Arg Glu Gly Glu Glu Gly Val Arg Leu Trp Thr Glu Gly Glu Lys Arg
223      195      200      205
226 Gln Leu Leu Ser Gly Arg Lys Val Leu Gly Tyr Asp Gly Tyr Tyr Val
227      210      215      220
230 Leu Ser Ile Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile
231 225      230      235      240
234 Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg
235      245      250
238 <210> SEQ ID NO: 4
240 <211> LENGTH: 252
242 <212> TYPE: PRT
244 <213> ORGANISM: Artificial Sequence
248 <220> FEATURE:
250 <223> OTHER INFORMATION: Mouse Ten M1
252 <400> SEQUENCE: 4
254 Met Ile Leu Gly Ile Gln Cys Glu Leu Gln Lys Gln Leu Arg Asn Phe
255 1      5      10      15
258 Ile Ser Leu Asp Gln Leu Pro Met Thr Pro Gln Tyr Asn Glu Gly Arg
259      20      25      30
262 Cys Leu Glu Gly Gly Lys Gln Pro Arg Phe Ala Ala Val Pro Ser Val
263      35      40      45
266 Phe Gly Lys Gly Ile Lys Phe Ala Ile Lys Glu Gly Ile Val Thr Ala
267      50      55      60
270 Asp Ile Ile Gly Val Ala Asn Glu Asp Ser Arg Arg Leu Ala Ala Ile
271 65      70      75      80
274 Leu Asn Asn Ala His Tyr Leu Glu Asn Leu His Phe Thr Ile Glu Gly
275      85      90      95
278 Arg Asp Thr His Tyr Phe Ile Lys Leu Gly Ser Leu Glu Glu Asp Leu
279      100     105     110
282 Val Leu Ile Gly Asn Thr Gly Gly Arg Arg Ile Leu Glu Asn Gly Val
283      115     120     125
286 Asn Val Thr Val Ser Gln Met Thr Ser Val Leu Asn Gly Arg Thr Arg
287      130     135     140
290 Arg Phe Ala Asp Ile Gln Leu Gln His Gly Ala Leu Cys Phe Asn Ile
291 145     150     155     160
294 Arg Tyr Gly Thr Thr Val Glu Glu Glu Lys Asn His Val Leu Glu Met
295      165     170     175
298 Ala Arg Gln Arg Ala Val Ala Gln Ala Trp Thr Gln Glu Gln Arg Arg
299      180     185     190
302 Leu Gln Glu Gly Glu Glu Gly Thr Arg Val Trp Thr Glu Gly Glu Lys
303      195     200     205

```

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```

306 Gln Gln Leu Leu Gly Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe
307      210                      215                      220
310 Val Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn
311 225                      230                      235                      240
314 Ile His Phe Met Arg Gln Ser Glu Ile Gly Arg Arg
315      245                      250
318 <210> SEQ ID NO: 5
320 <211> LENGTH: 253
322 <212> TYPE: PRT
324 <213> ORGANISM: Artificial Sequence
328 <220> FEATURE:
330 <223> OTHER INFORMATION: Mouse Ten M2
332 <400> SEQUENCE: 5
334 Leu Ile Thr Gly Val Gln Gln Thr Thr Glu Arg His Asn Gln Ala Phe
335 1      5                      10                      15
338 Leu Ala Leu Glu Gly Gln Val Ile Thr Lys Lys Leu His Ala Ser Ile
339      20                      25                      30
342 Arg Glu Lys Ala Gly His Trp Phe Ala Thr Thr Thr Pro Ile Ile Gly
343      35                      40                      45
346 Lys Gly Ile Met Phe Ala Ile Lys Glu Gly Arg Val Thr Thr Gly Val
347      50                      55                      60
350 Ser Ser Ile Ala Ser Glu Asp Ser Arg Lys Val Ala Ser Val Leu Asn
351 65      70                      75                      80
354 Asn Ala Tyr Tyr Leu Asp Lys Met His Tyr Ser Ile Glu Gly Lys Asp
355      85                      90                      95
358 Thr His Tyr Phe Val Lys Ile Gly Ala Ala Asp Gly Asp Leu Val Thr
359      100                     105                     110
362 Leu Gly Thr Thr Ile Gly Arg Lys Val Leu Glu Ser Gly Val Asn Val
363      115                     120                     125
366 Thr Val Ser Gln Pro Thr Leu Val Asn Gly Arg Thr Arg Arg Phe
367      130                     135                     140
370 Thr Asn Ile Glu Phe Gln Tyr Ser Thr Leu Leu Ser Ile Arg Tyr
371 145      150                     155                     160
374 Gly Leu Thr Pro Asp Thr Leu Asp Glu Glu Lys Ala Arg Val Leu Asp
375      165                     170                     175
378 Gln Ala Gly Gln Arg Ala Leu Gly Thr Ala Trp Ala Lys Glu Gln Gln
379      180                     185                     190
382 Lys Ala Arg Asp Gly Arg Glu Gly Ser Arg Leu Trp Thr Glu Gly Glu
383      195                     200                     205
386 Lys Gln Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr
387      210                     215                     220
390 Tyr Val Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser
391 225      230                     235                     240
394 Asn Ile Gln Phe Leu Arg Gln Asn Glu Met Gly Lys Arg
395      245                     250
398 <210> SEQ ID NO: 6
400 <211> LENGTH: 251
402 <212> TYPE: PRT
404 <213> ORGANISM: Artificial Sequence

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Input Set : A:\PTO.FG.txt

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408 &lt;220&gt; FEATURE:

410 &lt;223&gt; OTHER INFORMATION: Mouse Ten M3

412 &lt;400&gt; SEQUENCE: 6

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414 Pro Ile Phe Gly Val Gln Gln Gln Val Ala Arg Gln Ala Lys Ala Phe
415 1      5      10      15
418 Leu Ser Leu Gly Lys Met Ala Glu Val Gln Val Ser Arg Arg Lys Ala
419      20      25      30
422 Gly Ala Glu Gln Ser Trp Leu Trp Phe Ala Thr Val Lys Ser Leu Ile
423      35      40      45
426 Gly Lys Gly Val Met Leu Ala Val Ser Gln Gly Arg Val Gln Thr Asn
427      50      55      60
430 Val Leu Asn Ile Ala Asn Glu Asp Cys Ile Lys Val Ala Ala Val Leu
431 65      70      75      80
434 Asn Asn Ala Phe Tyr Leu Glu Asn Leu His Phe Thr Ile Glu Gly Lys
435      85      90      95
438 Asp Thr His Tyr Phe Ile Lys Thr Thr Thr Pro Glu Ser Asp Leu Gly
439      100      105      110
442 Thr Leu Arg Leu Thr Ser Gly Arg Lys Ala Leu Glu Asn Gly Ile Asn
443      115      120      125
446 Val Thr Val Ser Gln Ser Thr Thr Val Val Asn Gly Arg Thr Arg Arg
447      130      135      140
450 Phe Ala Asp Val Glu Met Gln Phe Gly Ala Leu Ala Leu His Val Arg
451 145      150      155      160
454 Tyr Gly Met Thr Leu Asp Glu Glu Lys Ala Arg Ile Leu Glu Gln Ala
455      165      170      175
458 Arg Gln Arg Ala Leu Ala Arg Ala Trp Ala Arg Glu Gln Gln Arg Val
459      180      185      190
462 Arg Asp Gly Glu Glu Gly Ala Arg Leu Trp Thr Glu Gly Glu Lys Arg
463      195      200      205
466 Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr Val
467      210      215      220
470 Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile
471 225      230      235      240
474 Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg
475      245      250

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478 &lt;210&gt; SEQ ID NO: 7

480 &lt;211&gt; LENGTH: 243

482 &lt;212&gt; TYPE: PRT

484 &lt;213&gt; ORGANISM: Artificial Sequence

488 &lt;220&gt; FEATURE:

490 &lt;223&gt; OTHER INFORMATION: Mouse Ten M4

492 &lt;400&gt; SEQUENCE: 7

```

494 Ser Ile Leu Gly Val Gln Cys Glu Val Gln Lys Gln Leu Lys Ala Phe
495 1      5      10      15
498 Val Thr Leu Glu Arg Phe Asp Gln Leu Tyr Gly Ser Thr Ile Thr Ser
499      20      25      30
502 Cys Gln Gln Ala Pro Glu Thr Lys Lys Phe Ala Ser Ser Gly Ser Ile
503      35      40      45
506 Phe Gly Lys Gly Val Lys Phe Ala Leu Lys Asp Gly Arg Val Thr Thr

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## RAW SEQUENCE LISTING ERROR SUMMARY

DATE: 11/08/2004

PATENT APPLICATION: US/10/510,959

TIME: 12:01:11

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\11082004\J510959.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:129; Xaa Pos. 1,3,4,5,6

Seq#:130; Xaa Pos. 1,2,3,4

Seq#:131; Xaa Pos. 2,3,4

Seq#:135; Xaa Pos. 5,6,9,19,32

## VERIFICATION SUMMARY

DATE: 11/08/2004

PATENT APPLICATION: US/10/510,959

TIME: 12:01:11

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\11082004\J510959.raw

L:19 M:270 C: Current Application Number differs, Replaced Application Number  
L:21 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:3903 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:129 after pos.:0  
L:3964 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:130 after pos.:0  
L:4015 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:131 after pos.:0  
L:4039 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:132,Line#:4035  
L:4799 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:133,Line#:4795  
L:4949 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:134,Line#:4945  
L:5109 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:135 after pos.:0  
M:341 Repeated in SeqNo=135